

In the Specification:

Please enter the Sequence Listing filed herewith.

Applicant presents replacement paragraphs below indicating the changes with insertions indicated by underlining and deletions indicated by strikeouts and/or double bracketing.

Please add the following section as the first section of the specification following the title.

Related Applications

This application is a national stage filing under 35 U.S.C. § 371 of PCT International application PCT/GB03/00030, filed January 7, 2003, which was published under PCT Article 21(2) in English.

On page 1, please add the following heading after the newly inserted Related Applications Section:

Field of the Invention

On page 1, line 7, please add the following heading:

Background of the Invention

On page 1, line 23, please insert the heading:

Summary of the Invention

On page 1, line 32, please insert the heading:

Description of the Preferred Embodiments

Please amend the paragraph that begins on page 5, line 1, as follows:

Oligonucleotides for use as NASBA P1 primers have the general structure "X₁-SEQ", wherein "X₁" represents a nucleotide sequence comprising a promoter and "SEQ" represents the HPV-specific sequence, as given in Table 1. The inclusion of a promoter sequence is essential in NASBA P1 primers but is not necessary in PCR primers, as discussed below. In a preferred embodiment, X₁ may be a sequence comprising a bacteriophage promoter, preferably the T7 promoter. In the most preferred embodiment, X₁ represents the sequence AATTCTAATACGACTCACTATAGGGAGAAGG (SEQ ID NO:385).

Please amend the paragraph that begins on page 8, line 16, as follows:

The first type of oligonucleotides are primer 1 oligonucleotides (also referred to herein as NASBA P1 primers), which are oligonucleotides of generally approximately 50 bases in length, containing an average of about 20 bases at the 3' end that are complementary to a region of the target mRNA. Oligonucleotides suitable for use as NASBA P1 primers are denoted "NASBA P1/PCR" in Table 1. The 5' ends of the P1 primer oligonucleotides (represented herein in general terms as X₁) comprise a promoter sequence that is recognized by a specific RNA polymerase. Bacteriophage promoters, for example the T7, T3 and SP6 promoters, are preferred for use in the oligonucleotides of the invention, since they provide advantages of high level transcription which is dependent only on binding of the appropriate RNA polymerase. In a preferred embodiment, the 5' terminal sequence of the P1 primer oligonucleotides may comprise the sequence AATTCTAATACGACTCACTATAGGG (SEQ ID NO:386) or the sequence AATTCTAATACGACTCACTATAGGGAGAAGG (SEQ ID NO:385). These sequences contains a T7 promoter, including the transcription initiation site for T7 RNA polymerase.

Please amend the paragraph that begins on page 10, line 2, as follows:

Oligonucleotides intended for use as NASBA P2 primers may, in a particular but non-limiting embodiment, further comprise a sequence of nucleotides at the 5' end which is unrelated to the target mRNA but which is capable of hybridising to a generic detection probe. The detection probe will preferably be labelled, for example with a fluorescent, luminescent or enzymatic label. In one embodiment the detection probe is labelled with a label that permits detection using ECL™ technology, although it will be appreciated that the invention is in no way limited to this particular method of detection. In a preferred embodiment the 5' end of the primer 2 oligonucleotides may comprise the sequence GATGCAAGGTCGCATATGAG (SEQ ID NO:387). This sequence is capable of hybridising to a generic ECL™ probe commercially available from Organon Teknika having the following structure:

$\text{Ru}(\text{bpy})_3^{2+}$ -GAT GCA AGG TCG CAT ATG AG-3' (SEQ ID NO:387)

Please amend the paragraph that begins on page 14, line 21, as follows:

Many examples of suitable pairs of quencher/fluorescer moieties which may be used in accordance with the invention are known in the art (see WO 95/13399, Tyagi and Kramer, *ibid*). A broad range of fluorophores in many different colours may be used, including for example 5-(2'-aminoethyl)aminonaphthalene-1-sulphonic acid (EDANS), fluorescein, FAM and Texas Red (see Tyagi, Bratu and Kramer, 1998, *Nature Biotechnology*, 16, 49-53). The use of probes labelled with different coloured fluorophores enables "multiplex" detection of two or more different probes in a single reaction vessel. A preferred quencher is 4-(4'-dimethylaminophenylazo)benzoic acid (DABCYL), a non-fluorescent chromophore, which serves as a 'universal' quencher for a wide range of fluorophores. The fluorescer and quencher moieties may be covalently attached to the probe in either orientation, either with the fluorescer at or near the 5' end and the quencher at or near the 3' end or vice versa. Protocols for the synthesis of molecular beacon probes are known in the art. A detailed protocol for synthesis is provided in a paper entitled "Molecular Beacons: Hybridization Probes for Detection of Nucleic Acids in Homogenous Solutions" by Sanjay Tyagi et al., Department of Molecular Genetics,

Public Health Research Institute, 455 First Avenue, New York, NY 10016, USA, which is available online via the PHRI website (at www-phri.nyu.edu or www.molecular-beacons.org).

Please amend the paragraph that begins on page 17, line 9, as follows:

The NASBA P2 primers (p2) in Table 2 include the sequence GATGCAAGGTCGCATATGAG (SEQ ID NO:387) at the 5' end; the NASBA P1 primers (p1) in Table 2 include the sequence AATTCTAATACGACTCACTATAGGGAGAAGG (SEQ ID NO:385) at the 5' end. Oligonucleotides suitable for use as probes are identified by "po". The P2 primers generally contain HPV sequences from the positive strand, whereas the p1 primers generally contain HPV sequences from the negative strand. nt-refers to nucleotide position in the relevant HPV genomic sequence.

Please amend Table 2, beginning on page 17, to add a column containing sequence identifiers (SEQ ID NOs) for the primer sequences, as follows:

Primer name	Sequence	SEQ ID NO	HPV Type	nt
HAe6701p2	GATGCAAGGTCGCATATGAGCCACAGGAGCGACCC AGAAAAGTTA	<u>134</u>	16	116
HAe6701p1	AATTCTAATACGACTCACTATAGGGAGAAGGACGG TTTGTTGTATTGCTGTTC	<u>135</u>	16	368
HAe6702p2	GATGCAAGGTCGCATATGAGCCACAGGAGCGACCC AGAAA	<u>136</u>	16	116
HAe6702p1	AATTCTAATACGACTCACTATAGGGAGAAGGGGTT TGTGTATTGCTGTTC	<u>137</u>	16	368
HAe6702Ap1	AATTCTAATACGACTCACTATAGGGAGAAGGTCA CGTCGCAGTAACTGT	<u>138</u>	16	208
HAe6702Bp1	AATTCTAATACGACTCACTATAGGGAGAAGGTTG CTTGCAGTACACACA	<u>139</u>	16	191
HAe6702Cp1	AATTCTAATACGACTCACTATAGGGAGAAGGTGC AGTACACACATTCTA	<u>140</u>	16	186
HAe6702Dp1	AATTCTAATACGACTCACTATAGGGAGAAGGGCA GTACACACATTCTAA	<u>141</u>	16	185
H16e6702Ap 2	GATGCAAGGTCGCATATGAGACAGTTATGCACAGA GCT	<u>142</u>	16	142
H16e6702Bp 2	GATGCAAGGTCGCATATGAGATATTAGAAATGTGTG TAC	<u>143</u>	16	182

H16e6702Cp 2	GATGCAAGGTCGCATATGAGTTAGAATGTGTGTAC TGC	<u>144</u>	16	185
H16e6702Dp 2	GATGCAAGGTCGCATATGAGGAATGTGTGTACTGC AAG	<u>145</u>	16	188
H16e6702Ap o	ACAGTTATGCACAGAGCT	<u>146</u>	16	142
H16e6702Bp o	ATATTAGAATGTGTGTAC	<u>147</u>	16	182
H16e6702Cp o	TTAGAATGTGTGTACTGC	<u>148</u>	16	185
H16e6702Dp o	GAATGTGTGTACTGCAAG	<u>149</u>	16	188
HAe6701po	CTTTGCTTTTCGGGATTTATGC	<u>150</u>	16	235
HAe6702po	TATGACTTTGCTTTTCGGGA	<u>151</u>	16	230
HAe6702mb1	X ₂ -cgcatgTATGACTTTGCTTTTCGGGAcatgcg -X ₃	<u>152</u>	16	230
HAe6702mb2	X ₂ -ccagctTATGACTTTGCTTTTCGGGAagctgg -X ₃	<u>153</u>	16	230
HAe6702mb3	X ₂ -cacgctTATGACTTTGCTTTTCGGGAgcgtg -X ₃	<u>154</u>	16	230
H16e6702mb 4	X ₂ -cgatcgTATGACTTTGCTTTTCGGGAcgcg -X ₃	<u>155</u>	16	230
HAe6703p2	GATGCAAGGTCGCATATGAGCAGAGGAGGAGGATG AAATAGTA	<u>156</u>	16	656
HAe6703p1	AATTCTAATACGACTCACTATAGGGAGAAGGGCAC AACCGAAGCGTAGAGTCACAC	<u>157</u>	16	741
HAe6703po	TGGACAAGCAGAACCGGACAGAGC	<u>158</u>	16	687
HAe6704p2	GATGCAAGGTCGCATATGAGCAGAGGAGGAGGATG AAATAGA	<u>159</u>	16	656
HAe6704p1	AATTCTAATACGACTCACTATAGGGAGAAGGGCAC AACCGAAGCGTAGAGTCA	<u>160</u>	16	741
HAe6704po	AGCAGAACCGGACAGAGCCCATTA	<u>161</u>	16	693
H18e6701p2	GATGCAAGGTCGCATATGAGACGATGAAATAGATG GAGTT	<u>162</u>	18	702
H18e6701p1	AATTCTAATACGACTCACTATAGGGAGAAGGCACG GACACACAAAGGACAG	<u>163</u>	18	869
H18e6701po	AGCCGAACCACAACGTCACA	<u>164</u>	18	748
H18e6702p2	GATGCAAGGTCGCATATGAGGAAAACGATGAAATA GATGGAG	<u>165</u>	18	698
H18e6702p1	AATTCTAATACGACTCACTATAGGGAGAAGGACAC CACGGACACACAAAGGACAG	<u>166</u>	18	869
H18e6702po	GAACCACAACGTCACACAATG	<u>167</u>	18	752
H18e6702mb 1	X ₂ - cgcatgGAACCACAACGTCACACAATGcatgcg -X ₃	<u>168</u>	18	752
H18e6702mb 2	X ₂ - ccgtcgGAACCACAACGTCACACAATGcgacgg -X ₃	<u>169</u>	18	752
H18e6702mb 3	X ₂ - cggaccGAACCACAACGTCACACAATGggtccg	<u>170</u>	18	752

	-X ₃			
H18e6702mb 4	X ₂ - cgatcgGAACCACAACGTCACACAATGcgatcg -X ₃	<u>171</u>	18	752
H18e6703p2	GATGCAAGGTCGCATATGAGTTCCGGTTGACCTTC TATGT	<u>172</u>	18	651
H18e6703p1	AATTCTAATACGACTCACTATAGGGAGAAGGGGTC GTCTGCTGAGCTTTCT	<u>173</u>	18	817
H18e6704p2	GATGCAAGGTCGCATATGAGGCAAGACATAGAAAT AACCTG	<u>174</u>	18	179
H18e6704p1	AATTCTAATACGACTCACTATAGGGAGAAGGACCC AGTGTTAGTTAGTT	<u>175</u>	18	379
H18e6704po	TGCAAGACAGTATTGGAACT	<u>176</u>	18	207
H31e6701p2	GATGCAAGGTCGCATATGAGGGAAATACCCTACGA TGAAC	<u>177</u>	31	164
H31e6701p1	AATTCTAATACGACTCACTATAGGGAGAAGGGGAC ACAACGGTCTTTGACA	<u>178</u>	31	423
H31e6701po	ATAGGGACGACACACCACACGGAG	<u>179</u>	31	268
H31e6702p2	GATGCAAGGTCGCATATGAGGGAAATACCCTACGA TGAAC	<u>180</u>	31	164
H31e6702p1	AATTCTAATACGACTCACTATAGGGAGAAGGCTGG ACACAACGGTCTTTGACA	<u>181</u>	31	423
H31e6702po	TAGGGACGACACACCACACGGA	<u>182</u>	31	269
H31e6703p2	GATGCAAGGTCGCATATGAGACTGACCTCCACTGT TATGA	<u>183</u>	31	617
H31e6703p1	AATTCTAATACGACTCACTATAGGGAGAAGGTATC TACTTGTGTGCTCTGT	<u>184</u>	31	766
H31e6703po	GACAAGCAGAACCGGACACATC	<u>185</u>	31	687
H31e6704p2	GATGCAAGGTCGCATATGAGTGACCTCCACTGTTA TGAGCAATT	<u>186</u>	31	619
H31e6704p1	AATTCTAATACGACTCACTATAGGGAGAAGGTGCG AATATCTACTTGTGTGCTCT GT	<u>187</u>	31	766
H31e6704po	GGACAAGCAGAACCGGACACATCCAA	<u>188</u>	31	686
H31e6704mb 1	X ₂ -ccgaaggGGACAAGCAGAACCGGACACATCC AAccttcgg -X ₃	<u>189</u>	31	686
H31e6704mb 2	X ₂ -ccgtcggGACAAGCAGAACCGGACACATCCA Acgacgg -X ₃	<u>190</u>	31	686
H31e6704mb 3	X ₂ - cacgtcggGACAAGCAGAACCGGACACATCCAA cgacgtg -X ₃	<u>191</u>	31	686
H31e6704mb 4	X ₂ -cgcagcGGACAAGCAGAACCGGACACATCCAA gctgcg -X ₃	<u>192</u>	31	686
H31e6704mb 5	X ₂ -cgatcggGACAAGCAGAACCGGACACATCCAA cgatcg -X ₃	<u>193</u>	31	686
H31e6705p2	GATGCAAGGTCGCATATGAGACTGACCTCCACTGT TAT	<u>194</u>	31	617
H31e6705p1	AATTCTAATACGACTCACTATAGGGAGAAGGCACG ATTCCAAATGAGCCCAT	<u>195</u>	31	809
H33e6701p2	GATGCAAGGTCGCATATGAGTATCCTGAACCAACT GACCTAT	<u>196</u>	33	618
H33e6701p1	AATTCTAATACGACTCACTATAGGGAGAAGGTTGA	<u>197</u>	33	763

	CACATAAACGAACTG			
H33e6701po	CAGATGGACAAGCACAACC	<u>198</u>	33	694
H33e6703p2	GATGCAAGGTCGCATATGAGTCTGAACCAACTGACCTAT	<u>199</u>	33	620
H33e6703p1	AATTCTAATACGACTCACTATAGGGAGAAGGCCCA TAAGTAGTTGCTGTAT	<u>200</u>	33	807
H33e6703po	GGACAAGCACAACCAGCCACAGC	<u>201</u>	33	699
H33e6703mb 1	X ₂ -ccaagcGGACAAGCACAACCAGCCACAGCgct tgg -X ₃	<u>202</u>	33	699
H33e6703mb 2	X ₂ -ccaagcggGACAAGCACAACCAGCCACAGC cgcttgg -X ₃	<u>203</u>	33	699
H33e6703mb 3	X ₂ -cccagcGGACAAGCACAACCAGCCACAGCgct ggg -X ₃	<u>204</u>	33	699
H33e6703mb 4	X ₂ -ccaaagcGGACAAGCACAACCAGCCACAGCg ctttgg -X ₃	<u>205</u>	33	699
H33e6703mb 5	X ₂ - cctgcGGACAAGCACAACCAGCCACAGCgcagg -X ₃	<u>206</u>	33	699
H33e6703mb 6	X ₂ -cgatcgGGACAAGCACAACCAGCCACAGCcga tcg -X ₃	<u>207</u>	33	699
H33e6702p2	GATGCAAGGTCGCATATGAGGACCTTTGTGTCTC AAGAA	<u>208</u>	33	431
H33e6702p1	AATTCTAATACGACTCACTATAGGGAGAAGGAGGT CAGTTGGTTCAGGATA	<u>209</u>	33	618
H33e6702po	AGAAACTGCACTGTGACGTGT	<u>210</u>	33	543
H35e6701p2	GATGCAAGGTCGCATATGAGATTACAGCGGAGTGA GGTAT	<u>211</u>	35	217
H35e6701p1	AATTCTAATACGACTCACTATAGGGAGAAGGGTCT TTGCTTTTCAACTGGA	<u>212</u>	35	442
H35e6701po	ATAGAGAAGGCCAGCCATAT	<u>213</u>	35	270
H35e6702p2	GATGCAAGGTCGCATATGAGTCAGAGGAGGAGGAA GATACTA	<u>214</u>	35	655
H35e6702p1	AATTCTAATACGACTCACTATAGGGAGAAGGGATT ATGCTCTCTGTGAACA	<u>215</u>	35	844
H35e6703p2	GATGCAAGGTCGCATATGAGCCCCAGGCCAACTGAC CTATA	<u>216</u>	35	610
H35e6703p1	AATTCTAATACGACTCACTATAGGGAGAAGGGTCA ATGTGTGTGCTCTGTA	<u>217</u>	35	770
H35e6702po	GACAAGCAAAAACCAGACACCTCCAA	<u>218</u>	35	692
H35e6703po	GACAAGCAAAAACCAGACACC	<u>219</u>	35	692
H52e6701p2	GATGCAAGGTCGCATATGAGTTGTGTGAGGTGCTG GAAGAAT	<u>220</u>	52	144
H52e6701p1	AATTCTAATACGACTCACTATAGGGAGAAGGCCCT CTCTTCTAATGTTT	<u>221</u>	52	358
H52e6701po	GTGCCTACGCTTTTTATCTA	<u>222</u>	52	296
H52e6702p2	GATGCAAGGTCGCATATGAGGTGCCTACGCTTTTT ATCTA	<u>223</u>	52	296
H52e6702p1	AATTCTAATACGACTCACTATAGGGAGAAGGGGGG TCTCCAACACTCTGAACA	<u>224</u>	52	507
H52e6702po	TGCAAAACAAGCGATTTC	<u>225</u>	52	461
H58e6701p2	GATGCAAGGTCGCATATGAGTCAGGCGTTGGAGAC	<u>226</u>	58	157

	ATC			
H58e6701p1	AATTCTAATACGACTCACTATAGGGAGAAGGAGCA ATCGTAAGCACACT	<u>227</u>	58	301
H58e6702p2	GATGCAAGGTCGCATATGAGTCTGTGCATGAAATC GAA	<u>228</u>	58	173
H58e6702p1	AATTCTAATACGACTCACTATAGGGAGAAGGAGCA CACTTTACATACTG	<u>229</u>	58	291
H58e6701po	TGAAATGCGTTGAATGCA	<u>230</u>	58	192
H58e6702po	TTGCAGCGATCTGAGGTATATG	<u>231</u>	58	218
HBe6701p2	GATGCAAGGTCGCATATGAGTACACTGCTGGACAA CAT	<u>232</u>	B(11)	514
HBe6701p1	AATTCTAATACGACTCACTATAGGGAGAAGGTCAT CTTCTGAGCTGTCT	<u>233</u>	B(11)	619
HBe6702p2	GATGCAAGGTCGCATATGAGTACACTGCTGGACAA CATGCA	<u>234</u>	B(11)	514
HBe6702p1	AATTCTAATACGACTCACTATAGGGAGAAGGGTCA CATCCACAGCAACAGGTCA	<u>235</u>	B(11)	693
HBe6701po	GTAGGGTTACATTGCTATGA	<u>236</u>	B(11)	590
HBe6702po	GTAGGGTTACATTGCTATGAGC	<u>237</u>	B(11)	590
HBe6703p2	GATGCAAGGTCGCATATGAGTGACCTGTTGCTGTG GATGTGA	<u>238</u>	B(11)	693
HBe6703p1	AATTCTAATACGACTCACTATAGGGAGAAGGTACC TGAATCGTCCGCCAT	<u>239</u>	B(11)	832
HBe6703po	ATWGTGTGTCCCATCTGC	<u>240</u>	B(11)	794
HCe6701p2	GATGCAAGGTCGCATATGAGCATGCCATAAATGTA TAGA	<u>241</u>	C(18 39 45)	295
HCe6701p1	AATTCTAATACGACTCACTATAGGGAGAAGGCACC GCAGGCACCTTATTAA	<u>242</u>	C(18 39 45)	408
HCe6701po	AGAATTAGAGAATTAAGA	<u>243</u>	C(18 39 45)	324
H39e6701p2	GATGCAAGGTCGCATATGAGGCAGACGACCACTAC AGCAAA	<u>244</u>	39	210
H39e6701p1	AATTCTAATACGACTCACTATAGGGAGAAGGACAC CGAGTCCGAGTAATA	<u>245</u>	39	344
H39e6701po	ATAGGGACGGGGAACCACT	<u>246</u>	39	273
H39e6702p2	GATGCAAGGTCGCATATGAGTATTACTCGGACTCG GTGT	<u>247</u>	39	344
H39e6702p1	AATTCTAATACGACTCACTATAGGGAGAAGGCTTG GGTTTCTCTTCGTGTTA	<u>248</u>	39	558
H39e6702po	GGACCACAAAACGGGAGGAC	<u>249</u>	39	531
H39e6703p2	GATGCAAGGTCGCATATGAGGAAATAGATGAACCC GACCA	<u>250</u>	39	703
H39e6703p1	AATTCTAATACGACTCACTATAGGGAGAAGGGCAC ACCACGGACACACAAA	<u>251</u>	39	886
H39e6703po	TAGCCAGACGGGATGAACCACAGC	<u>252</u>	39	749
H45e6701p2	GATGCAAGGTCGCATATGAGAACCATTGAACCCAG CAGAAA	<u>253</u>	45	430
H45e6701p1	AATTCTAATACGACTCACTATAGGGAGAAGGTCTT TCTTGCCGTGCCTGGTCA	<u>254</u>	45	527
H45e6702p2	GATGCAAGGTCGCATATGAGGAAACCATTGAACCC AGCAGAAAA	<u>255</u>	45	428

H45e6702p1	AATTCTAATACGACTCACTATAGGGAGAAGGTTGC TATACTTGTGTTTCCCTACG	<u>256</u>	45	558
H45e6701po	GTACCGAGGGCAGTGTAATA	<u>257</u>	45	500
H45e6702po	GGACAAACGAAGATTTTCA	<u>258</u>	45	467
H45e6703p2	GATGCAAGGTCGCATATGAGGTTGACCTGTTGTGT TACCAGCAAT	<u>259</u>	45	656
H45e6703p1	AATTCTAATACGACTCACTATAGGGAGAAGGCACC ACGGACACACAAAGGACAAG	<u>260</u>	45	868
H45e6704p2	GATGCAAGGTCGCATATGAGCTGTTGACCTGTTGT GTTACGA	<u>261</u>	45	654
H45e6704p1	AATTCTAATACGACTCACTATAGGGAGAAGGCCAC GGACACACAAAGGACAAG	<u>262</u>	45	868
H45e6705p2	GATGCAAGGTCGCATATGAGGTTGACCTGTTGTGT TACGA	<u>263</u>	45	656
H45e6705p1	AATTCTAATACGACTCACTATAGGGAGAAGGACGG ACACACAAAGGACAAG	<u>264</u>	45	868
H45e6703po	GAGTCAGAGGAGGAAAACGATG	<u>265</u>	45	686
H45e6704po	AGGAAAACGATGAAGCAGATGGAGT	<u>266</u>	45	696
H45e6705po	ACAAC TACCAGCCC GACGAGCCGAA	<u>267</u>	45	730
H51e6701p2	GATGCAAGGTCGCATATGAGGGAGGAGGATGAAGT AGATA	<u>268</u>	51	658
H51e6701p1	AATTCTAATACGACTCACTATAGGGAGAAGGGCCC ATTAACATCTGCTGTA	<u>269</u>	51	807
H51e6702p2	GATGCAAGGTCGCATATGAGAGAGGAGGAGGATGA AGTAGATA	<u>270</u>	51	655
H51e6702p1	AATTCTAATACGACTCACTATAGGGAGAAGGACGG GCAAACCAGGCTTAGT	<u>271</u>	51	829
H51e6701po	GCAGGTGTTCAAGTGTAGTA	<u>272</u>	51	747
H51e6702po	TGGCAGTGGAAAGCAGTGGAGACA	<u>273</u>	51	771
H56e6701p2	GATGCAAGGTCGCATATGAGTTGGGGTGCTGGAGA CAAACATCT	<u>274</u>	56	519
H56e6701p1	AATTCTAATACGACTCACTATAGGGAGAAGGTTCA TCCTCATCCTCATCCTCTGA	<u>275</u>	56	665
H56e6702p2	GATGCAAGGTCGCATATGAGTGGGGTGCTGGAGAC AAACATC	<u>276</u>	56	520
H56e6702p1	AATTCTAATACGACTCACTATAGGGAGAAGGCATC CTCATCCTCATCCTCTGA	<u>277</u>	56	665
H56e6703p2	GATGCAAGGTCGCATATGAGTTGGGGTGCTGGAGA CAAACAT	<u>278</u>	56	519
H56e6703p1	AATTCTAATACGACTCACTATAGGGAGAAGGCCAC AAACTTACACTCACAACA	<u>279</u>	56	764
H56e6701po	AAAGTACCAACGCTGCAAGACGT	<u>280</u>	56	581
H56e6702po	AGAACTAACACCTCAAACAGAAAT	<u>281</u>	56	610
H56e6703po	AGTACCAACGCTGCAAGACGTT	<u>282</u>	56	583
H56e6703po 1	TTGGACAGCTCAGAGGATGAGG	<u>283</u>	56	656
H56e6704p2	GATGCAAGGTCGCATATGAGGATTTTCTTATGCA GTGTG	<u>284</u>	56	279
H56e6704p1	AATTCTAATACGACTCACTATAGGGAGAAGGGACA TCTGTAGCACCTTATT	<u>285</u>	56	410
H56e6704po	GACTATTCAAGTGTATGGAGC	<u>286</u>	56	348

HPVAP01A	CAACTGAYCTMYACTGTTATGA	<u>287</u>	A (16 31 35)	
HPVAp01Amb 1	X ₂ - cgcatgCAACTGAYCTMYACTGTTATGAcatgcg -X ₃	<u>288</u>	A (16 31 35)	
HPVAp01Amb 2	X ₂ -ccgtcgCAACTGAYCTMYACTGTTATGAcga cgg -X ₃	<u>289</u>	A (16 31 35)	
HPVAp01Amb 3	X ₂ -ccacccCAACTGAYCTMYACTGTTATGAgg gtgg -X ₃	<u>290</u>	A (16 31 35)	
HPVAp01Amb 4	X ₂ -cgatcgCAACTGAYCTMYACTGTTATGAcga tcg -X ₃	<u>291</u>	A (16 31 35)	
HPVAP04A	GAAMCAACTGACCTAYWCTGCTAT	<u>292</u>	A (33 52 58)	
HPVAP04Amb 1	X ₂ -ccaagcGAAMCAACTGACCTAYWCTGCTATgc ttgg -X ₃	<u>293</u>	A (33 52 58)	
HPVAP04Amb 2	X ₂ -ccaagccGAAMCAACTGACCTAYWCTGCTAT ggcttgg -X ₃	<u>294</u>	A (33 52 58)	
HPVAP04Amb 3	X ₂ -ccaagcgGAAMCAACTGACCTAYWCTGCTA Tcgcttgg -X ₃	<u>295</u>	A (33 52 58)	
HPVAP04Amb 4	X ₂ -ccagcgGAAMCAACTGACCTAYWCTGCTATcg ctgg -X ₃	<u>296</u>	A (33 52 58)	
HPVAP04Amb 5	X ₂ -cgatcgGAAMCAACTGACCTAYWCTGCTATcg atcg -X ₃	<u>297</u>	A (33 52 58)	
HPVCPO4	AAGACATTATTCAGACTC	<u>298</u>	C (18 45 39)	
HPVCPO4Amb 1	X ₂ -ccaagcAAGACATTATTCAGACTCgcttgg -X ₃	<u>299</u>	C (18 45 39)	
HPVCPO4Amb 2	X ₂ -cgcatgAAGACATTATTCAGACTCcatgcg -X ₃	<u>300</u>	C (18 45 39)	
HPVCPO4Amb 3	X ₂ -cccagcAAGACATTATTCAGACTCgctggg -X ₃	<u>301</u>	C (18 45 39)	
HPVCPO4Amb 4	X ₂ -cgatcgAAGACATTATTCAGACTCcgatcg -X ₃	<u>302</u>	C (18 45 39)	

Please amend Table 3, beginning on page 22, to add a column containing sequence identifiers (SEQ ID NOs) for the primer sequences, as follows:

Primer name	Sequence	<u>SEQ ID NO</u>	HPV type	nt
HAe6701PCR2	CCACAGGAGCGACCCAGAAAGTTA	<u>303</u>	16	116
HAe6701PCR1	ACGGTTTGTGTATTGCTGTTC	<u>304</u>	16	368
HAe6702PCR2	CCACAGGAGCGACCCAGAAA	<u>305</u>	16	116
HAe6702PCR1	GGTTTGTGTATTGCTGTTC	<u>306</u>	16	368
HAe6703PCR2	CAGAGGAGGAGGATGAAATAGTA	<u>307</u>	16	656
HAe6703PCR1	GCACAACCGAAGCGTAGAGTCACAC	<u>308</u>	16	741
HAe6704PCR2	CAGAGGAGGAGGATGAAATAGA	<u>309</u>	16	656
HAe6704PCR1	GCACAACCGAAGCGTAGAGTCA	<u>310</u>	16	741
H18e6701PCR2	ACGATGAAATAGATGGAGTT	<u>311</u>	18	702

H18e6701PCR1	CACGGACACACAAAGGACAG	<u>312</u>	18	869
H18e6702PCR2	GAAAACGATGAAATAGATGGAG	<u>313</u>	18	698
H18e6702PCR1	ACACCACGGACACACAAAGGACAG	<u>314</u>	18	869
H18e6703PCR2	TTCCGGTTGACCTTCTATGT	<u>315</u>	18	651
H18e6703PCR1	GGTCGTCTGCTGAGCTTTCT	<u>316</u>	18	817
H18e6704PCR2	GCAAGACATAGAAATAACCTG	<u>317</u>	18	179
H18e6704PCR1	ACCCAGTGTTAGTTAGTT	<u>318</u>	18	379
H31e6701PCR2	GGAAATACCCTACGATGAAC	<u>319</u>	31	164
H31e6701PCR1	GGACACAACGGTCTTTGACA	<u>320</u>	31	423
H31e6702PCR2	GGAAATACCCTACGATGAACATA	<u>321</u>	31	164
H31e6702PCR1	CTGGACACAACGGTCTTTGACA	<u>322</u>	31	423
H31e6703PCR2	ACTGACCTCCACTGTTATGA	<u>323</u>	31	617
H31e6703PCR1	TATCTACTTGTGTGCTCTGT	<u>324</u>	31	766
H31e6704PCR2	TGACCTCCACTGTTATGAGCAATT	<u>325</u>	31	619
H31e6704PCR1	TGCGAATATCTACTTGTGTGCTCT GT	<u>326</u>	31	766
H31e6705PCR2	ACTGACCTCCACTGTTAT	<u>327</u>	31	617
H31e6705PCR1	CACGATTCCAAATGAGCCCAT	<u>328</u>	31	809
H33e6701PCR2	TATCCTGAACCAACTGACCTAT	<u>329</u>	33	618
H33e6701PCR1	TTGACACATAAACGAACATG	<u>330</u>	33	763
H33e6703PCR2	TCCTGAACCAACTGACCTAT	<u>331</u>	33	620
H33e6703PCR1	CCCATAAGTAGTTGCTGTAT	<u>332</u>	33	807
H33e6702PCR2	GACCTTTGTGTCCTCAAGAA	<u>333</u>	33	431
H33e6702PCR1	AGGTCAGTTGGTTCAGGATA	<u>334</u>	33	618
H35e6701PCR2	ATTACAGCGGAGTGAGGTAT	<u>335</u>	35	217
H35e6701PCR1	GTCTTTGCTTTTCAACTGGA	<u>336</u>	35	442
H35e6702PCR2	TCAGAGGAGGAGGAAGATACTA	<u>337</u>	35	655
H35e6702PCR1	GATTATGCTCTCTGTGAACA	<u>338</u>	35	844
H35e6703PCR2	CCCAGGCAACTGACCTATA	<u>339</u>	35	610
H35e6703PCR1	GTCAATGTGTGTGCTCTGTA	<u>340</u>	35	770
H52e6701PCR2	TTGTGTGAGGTGCTGGAAGAAT	<u>341</u>	52	144
H52e6701PCR1	CCCTCTCTTCTAATGTTT	<u>342</u>	52	358
H52e6702PCR2	GTGCCTACGCTTTTTATCTA	<u>343</u>	52	296
H52e6702PCR1	GGGGTCTCCAACACTCTGAACA	<u>344</u>	52	507
H58e6701PCR2	TCAGGCGTTGGAGACATC	<u>345</u>	58	157
H58e6701PCR1	AGCAATCGTAAGCACACT	<u>346</u>	58	301
H58e6702PCR2	TCTGTGCATGAAATCGAA	<u>347</u>	58	173
H58e6702PCR1	AGCACACTTTACATACTG	<u>348</u>	58	291
HBe6701PCR2	TACACTGCTGGACAACAT	<u>349</u>	B (11)	514
HBe6701PCR1	TCATCTTCTGAGCTGTCT	<u>350</u>	B (11)	619
HBe6702PCR2	TACACTGCTGGACAACATGCA	<u>351</u>	B (11)	514
HBe6702PCR1	GTCACATCCACAGCAACAGGTCA	<u>352</u>	B (11)	693
HBe6703PCR2	TGACCTGTTGCTGTGGATGTGA	<u>353</u>	B (11)	693
HBe6703PCR1	TACCTGAATCGTCCGCCAT	<u>354</u>	B (11)	832
HCe6701PCR2	CATGCCATAAATGTATAGA	<u>355</u>	C (18 39 45)	295
HCe6701PCR1	CACCGCAGGCACCTTATTAA	<u>356</u>	C (18 39 45)	408
H39e6701PCR2	GCAGACGACCACTACAGCAAA	<u>357</u>	39	210
H39e6701PCR1	ACACCGAGTCCGAGTAATA	<u>358</u>	39	344

H39e6702PCR2	TATTACTCGGACTCGGTGT	<u>359</u>	39	344
H39e6702PCR1	CTTGGGTTTCTCTTCGTGTTA	<u>360</u>	39	558
H39e6703PCR2	GAAATAGATGAACCCGACCA	<u>361</u>	39	703
H39e6703PCR1	GCACACCACGGACACACAAA	<u>362</u>	39	886
H45e6701PCR2	AACCATTGAACCCAGCAGAAA	<u>363</u>	45	430
H45e6701PCR1	TCTTTCTTGCCGTGCCTGGTCA	<u>364</u>	45	527
H45e6702PCR2	GAAACCATTGAACCCAGCAGAAA	<u>365</u>	45	428
H45e6702PCR1	TTGCTATACTTGTGTTTCCCTACG	<u>366</u>	45	558
H45e6703PCR2	GTTGACCTGTTGTGTTACCAGCAAT	<u>367</u>	45	656
H45e6703PCR1	CACCACGGACACACAAAGGACAAG	<u>368</u>	45	868
H45e6704PCR2	CTGTTGACCTGTTGTGTTACGA	<u>369</u>	45	654
H45e6704PCR1	CCACGGACACACAAAGGACAAG	<u>370</u>	45	868
H45e6705PCR2	GTTGACCTGTTGTGTTACGA	<u>371</u>	45	656
H45e6705PCR1	ACGGACACACAAAGGACAAG	<u>372</u>	45	868
H51e6701PCR2	GGAGGAGGATGAAGTAGATA	<u>373</u>	51	658
H51e6701PCR1	GCCCATTAAACATCTGCTGTA	<u>374</u>	51	807
H51e6702PCR2	AGAGGAGGAGGATGAAGTAGATA	<u>375</u>	51	655
H51e6702PCR1	ACGGGCAAACCAGGCTTAGT	<u>376</u>	51	829
H56e6701PCR2	TTGGGGTGCTGGAGACAAACATCT	<u>377</u>	56	519
H56e6701PCR1	TTCATCCTCATCCTCATCCTCTGA	<u>378</u>	56	665
H56e6702PCR2	TGGGGTGCTGGAGACAAACATC	<u>379</u>	56	520
H56e6702PCR1	CATCCTCATCCTCATCCTCTGA	<u>380</u>	56	665
H56e6703PCR2	TTGGGGTGCTGGAGACAAACAT	<u>381</u>	56	519
H56e6703PCR1	CCACAACTTACACTACAACA	<u>382</u>	56	764
H56e6704PCR2	GATTTTCCTTATGCAGTGTG	<u>383</u>	56	279
H56e6704PCR1	GACATCTGTAGCACCTTATT	<u>384</u>	56	410